

RAW SEQUENCE LISTING

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Application Serial Number: 10/511, 468A
Source: PCF
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RAW SEQUENCE LISTING

DATE: 04/14/2006

PATENT APPLICATION: US/10/511,468A

TIME: 11:16:57

Input Set : A:\2005-11-21 4614-0159PUS1.ST25.txt

Output Set: N:\CRF4\04142006\J511468A.raw

5 <110> APPLICANT: Soren Weis DAHL et al.
 7 <120> TITLE OF INVENTION: TRANSLOCATION DEPENDENT COMPLEMENTATION FOR DRUG SCREENING
 9 <130> FILE REFERENCE: 4614-0159PUS1
 11 <140> CURRENT APPLICATION NUMBER: US 10/511,468A
 12 <141> CURRENT FILING DATE: 2004-10-18
 14 <160> NUMBER OF SEQ ID NOS: 99
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 238
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Aequorea victoria
 23 <400> SEQUENCE: 1
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 27 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 28 20 25 30
 30 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 31 35 40 45
 33 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 34 50 55 60
 36 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 37 65 70 75 80
 39 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 40 85 90 95
 42 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 43 100 105 110
 45 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 46 115 120 125
 48 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 49 130 135 140
 51 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 52 145 150 155 160
 54 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 55 165 170 175
 57 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 58 180 185 190
 60 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 61 195 200 205
 63 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 64 210 215 220
 66 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 67 225 230 235
 69 <210> SEQ ID NO: 2

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70 <211> LENGTH: 238

71 <212> TYPE: PRT

72 <213> ORGANISM: Aequorea victoria

74 <400> SEQUENCE: 2

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75 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
76 1          5          10          15
78 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
79          20          25          30
81 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
82          35          40          45
84 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
85          50          55          60
87 Ser Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
88 65          70          75          80
90 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
91          85          90          95
93 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
94          100         105         110
96 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
97          115         120         125
99 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
100         130         135         140
102 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
103 145         150         155         160
105 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
106         165         170         175
108 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
109         180         185         190
111 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
112         195         200         205
114 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
115         210         215         220
117 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
118 225         230         235

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120 <210> SEQ ID NO: 3

121 <211> LENGTH: 238

122 <212> TYPE: PRT

123 <213> ORGANISM: Aequorea victoria

125 <400> SEQUENCE: 3

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126 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
127 1          5          10          15
129 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
130          20          25          30
132 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
133          35          40          45
135 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
136          50          55          60
138 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
139 65          70          75          80

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141 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
142      85                      90                      95
144 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
145      100                    105                    110
147 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
148      115                    120                    125
150 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
151      130                    135                    140
153 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
154 145      150                    155                    160
156 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
157      165                    170                    175
159 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
160      180                    185                    190
162 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
163      195                    200                    205
165 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
166      210                    215                    220
168 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
169 225      230                    235
171 <210> SEQ ID NO: 4
172 <211> LENGTH: 239
173 <212> TYPE: PRT
174 <213> ORGANISM: Aequorea victoria
176 <400> SEQUENCE: 4
177 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
178 1      5                      10                      15
180 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
181      20                      25                      30
183 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
184      35                      40                      45
186 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
187      50                      55                      60
189 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
190 65      70                      75                      80
192 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
193      85                      90                      95
195 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
196      100                    105                    110
198 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
199      115                    120                    125
201 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
202      130                    135                    140
204 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
205 145      150                    155                    160
207 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
208      165                    170                    175
210 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
211      180                    185                    190

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213 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
214      195      200      205
216 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
217      210      215      220
219 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
220 225      230      235
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 239
224 <212> TYPE: PRT
225 <213> ORGANISM: Aequorea victoria
227 <400> SEQUENCE: 5
228 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
229 1      5      10      15
231 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
232      20      25      30
234 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
235      35      40      45
237 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
238      50      55      60
240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
241 65      70      75      80
243 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
244      85      90      95
246 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
247      100     105     110
249 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
250      115     120     125
252 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
253      130     135     140
255 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
256 145     150     155     160
258 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
259      165     170     175
261 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
262      180     185     190
264 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
265      195     200     205
267 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
268      210     215     220
270 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
271 225     230     235
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 239
275 <212> TYPE: PRT
276 <213> ORGANISM: Aequorea victoria
278 <400> SEQUENCE: 6
279 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
280 1      5      10      15
282 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

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```

283          20          25          30
285 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
286          35          40          45
288 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
289          50          55          60
291 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
292 65          70          75          80
294 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
295          85          90          95
297 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
298          100          105          110
301 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
302          115          120          125
304 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
305          130          135          140
307 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
308 145          150          155          160
310 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
311          165          170          175
313 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
314          180          185          190
316 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
317          195          200          205
319 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
320          210          215          220
322 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
323 225          230          235

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326 <210> SEQ ID NO: 7

327 <211> LENGTH: 121

328 <212> TYPE: DNA

329 <213> ORGANISM: Homo sapiens

331 <220> FEATURE:

332 <221> NAME/KEY: CDS

333 <222> LOCATION: (3)..(116)

335 <400> SEQUENCE: 7

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336 cc atg gcc ggt ggt acc ggt tcc ggt gcc ctg aag aag gag ctg cag      47
337   Met Ala Gly Gly Thr Gly Ser Gly Ala Leu Lys Lys Glu Leu Gln
338   1          5          10          15
340 gcc aac aag aag gag ctg gcc cag ctg aag tgg gag ctg cag gcc ctg      95
341 Ala Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu
342          20          25          30
344 aag aag gag ctg gcc cag tag gatcc      121
345 Lys Lys Glu Leu Ala Gln
346          35

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348 <210> SEQ ID NO: 8

349 <211> LENGTH: 37

350 <212> TYPE: PRT

351 <213> ORGANISM: Homo sapiens

353 <400> SEQUENCE: 8

VERIFICATION SUMMARY

DATE: 04/14/2006

PATENT APPLICATION: US/10/511,468A

TIME: 11:16:58

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